

CLAIMS

1. A method of transforming trees to modify the fibre characteristics in trees, the method comprising stably incorporating into the plant genome a chimaeric gene comprising a promoter and a nucleic acid coding sequence encoding a gene capable of modifying the extension of fibre cell walls, and regenerating a plant having an altered genome.
2. A method according to Claim 1, wherein said nucleic acid sequence encodes one or more of the class of proteins known as expansins.
3. A method according to Claim 1 or 2, wherein said nucleic acid sequence is derived from *Eucalyptus* or cucumber.
4. A method according to Claim 3, wherein said nucleic acid sequence is one or more of SEQ. ID. Nos. 1-6 hereof or the cucumber expansin sequence known herein as cucumber Ex29 (GenBank Accession No. U30382), or a sequence which has sufficient homology to hybridise to any one of SEQ. ID. Nos. 1-6 or cucumber Ex29 under medium stringency conditions (washing at 2x SSC at 65°C).
5. A method according to any one of the preceding claims, wherein said nucleic acid sequence is an mRNA, a cDNA sequence or a genomic DNA.

6. A method according to any one of Claims 1-5, wherein said chimaeric gene is in accordance with any one of Claims 8-13.
7. A nucleic acid coding sequence encoding a gene capable of modifying the extension of fibre cell walls, the nucleic acid coding sequence being one or more of SEQ. ID. Nos. 1-6 hereof, or a sequence which has sufficient homology to hybridise to any one of SEQ. ID. Nos. 1-6 under medium stringency conditions.
8. A chimaeric gene comprising a promoter and a nucleic acid sequence encoding a gene capable of modifying the extension of fibre cell walls, said nucleic acid sequence being one or more of SEQ. ID. Nos. 1-6 hereof, or a sequence which has sufficient homology to hybridise thereto under medium stringency conditions.
9. A chimaeric gene according to Claim 6 or 8, wherein said chimaeric gene further comprises a terminator.
10. A chimaeric gene according to Claim 6, 8 or 9, wherein said chimaeric gene comprises said nucleic acid coding sequence as said nucleic acid sequence exists in nature, complete with endogenous promoter, terminator, introns and other regulatory sequences.
11. A chimaeric gene according to Claim 6, 8 or 9, wherein said chimaeric gene comprises said nucleic acid coding sequence, with or without introns, combined with a

heterologous promoter, terminator and/or other regulatory sequences.

12. A chimaeric gene according to any one of Claims 6 or 8-11, wherein said promoter is one of said group consisting of the cauliflower mosaic virus 35S promoter (CaMV35S), the cauliflower mosaic virus 19S promoter (CaMV19S), the nopaline synthase promoter, the *rolC*, patatin or *petE* promoters, or the AlcR/AlcS promoter.
13. A chimaeric gene according to any one of Claims 6 or 8-12, wherein said nucleic acid sequence, or parts thereof, is arranged in the normal reading frame direction or in the reverse reading frame direction.
14. A tree comprising a chimaeric gene according to any one of Claims 8-13.
15. A plant cell comprising a chimaeric gene according to any one of Claims 8-13.
16. A tree transformed according to the method of any one of Claims 1-7.
17. A tree according to Claim 16, said tree being a eucalypt, aspen, pine or larch.
18. A seed of a tree transformed according to the method of any one of Claims 1-7.